Homologous human p Human endotheliase Protein of human p Guinea pig AST pro Canine AST protein Amino acid sequenc Human SERS protein Hamster AST protein Rabbit AST protein Amino acid sequenc

Human endotheliase

Trypsin-like enzym Human lung tumour Human lung tumour Human lung tumour-Human lung tumour-Human lung tumour-

Porcine AST protein Bovine AST protein Macaca fasciculari

Human airway tryps Human airway speci Human AST SEQ ID N Human airway tryps

Sequence:

Run on:

Searched:

Database

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prostate cancer; head; neck;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19..37
/note= "Hydrophobic transmembrane region"
190..191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191..422
/note= "Catalytic domain"
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                                                                                                                                                                                                                            ABB06968
AAR89435
AAY29501
AAY29502
AAB44437
AAB44438
AAE13778
                                                                                                                                                                                                                                                                                                                                                                   ABB06964
ABB77355
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                                                                                                                                                                                                                                                                                                                                                                                                             AAY29498
AAB44428
AAE13769
ABB06965
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ABB06970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY94708 standard; Protein; 422 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DESC1 protein variant #1
 99WO-IB01818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0122747
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WO200050061-A1
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Domain
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Copyright (c) 1993 - 2003 Compugen Ltd.
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2 3 4 4 4 7 7 10 10

Result Š Lang JC;

Mouse airway speci Mouse AST SEQ ID N Novel human diagno Amino acid sequenc Protease PRTS-8.

Human lung tumour-Human lung tumour-Human lung tumour

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carcinoma or prostate cancer, comperising assaying for the expression of the DESCI gene in the tissue sample from a subject. The present sequence cereated the human DESCI protein variant I. The human DESCI gene is represents the human DESCI protein variant I. The human DESCI gene is located on chromosome 4q12-4q13, and the DESCI protein has a predicted molecular weight of 44kD. The DESCI gene is expressed in significant levels in epithelial derived tissue of the head, neck, oral mucosa, tonsils, prostate, testes and skin in healthy individuals. Tissue samples from patients with squamous cell carcinoma (particularly of the head and neck) do not express, or expresses at low levels the DESCI gene. Expression of the DESCI gene is reduced or absent in prostate cancer. The DESCI protein shows homology to serine protease family members. The methods of the invention can be used to diagnose squamous cell carcinoma useful for producing DESCI protein and for designing hybridization probes for isolating and identifying CDNA clones and genomic clones encoding the
                                                                          such
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                                                                                                                                                            This invention relates to a method for the diagnosis of squamous cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                         Diagnosing squamous cell carcinoma or prostate cancer especially squamous cell carcinomas of head and neck and tissues adjacent to tumor tissue comprises assaying for the expression of DESC1 gene
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Pred. No. 1.1e-178;
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                                                                                                                            Claim 8; Fig 1A; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                          protein or its allelic forms
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           WPI; 2000-572035/53
N-PSDB; AAA28125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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CODD; cancer; cardiovascular disease; nervous system disease; arrhythmia; congestive heart failure; myocardial infarction; ischaemic disease; hypertensive vascular disease; peripheral vascular disease; enzyme.
                                                             chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human DESC1-like serine proteases and polynucleotides encoding such proteins. DESC1-like serine proteases are discusseful for treating a DESC1-like serine protease dysfunction related disease conditions such as cancer, chronic obstructive pulmonary disease (CODD), cardiovascular diseases (e.g., myocardial infarction, congestive heart failure, isoheamic diseases of heart, all kinds of atrial and ventricular arrhythmias, hypertensive vascular diseases and peripheral vascular diseases and peripheral or central nervous system diseases. They are also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to the presence of mutations in the nucleic acid sequences which encode the enzyme. The present sequence is human DESC1-like serine protease
                                                                                                                                                                                                                                                                                                                                                                                                  useful for identifying
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Pred. No. 1.1e-178;
1; Mismatches 1;
                               Human DESC1-like serine protease homologue
                                                             DESC1-like serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 3; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%;
                                                                                                                                                                                                                                                                        18-JUL-2000; 2000US-218832P.
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 (first entry)
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17-MAY-2002
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AAE18723 standard; Protein; 422 AA

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17-NOV-1998;
  Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadheslon; pharmaceutical; screening.
                                                                                                                                                                                                                                                Human PRO1461 (UNQ742) amino acid sequence SEQ ID NO:269
                                                                                                                                                                       AAY99414 standard; Protein; 423 AA
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980S-0098749.
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                                                                                                                                                                                                                                                                         AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                       New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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Pred. No. 1.1e-178;
1; Mismatches 1;
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                                                                                                                                               Gurney AL,
            98US-0108925.
98US-0108849.
98US-0108850.
98US-0108851.
98US-0108851.
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Best Local Similarity 99.5%;
Matches 420; Conservative 1
  98US-0108867
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                                                                                                                                              Baker K, Goddard A,
                                                                                                                      (GETH ) GENENTECH INC
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N-PSDB; AAA37096.
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RESULT 4

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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
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                                                           mammal; tumour; cancer; human; cattle; horse; sheep;
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ng Z;
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Wood WI, Zhang
                                        Human PRO polypeptide sequence #160.
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Watanabe CK,
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2000US-198121P.
2000US-198585P.
2000US-199397P.
2000US-199550P.
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2000WO-US15264.
2000WO-US20710.
2000WS-0644848.
2000WO-US23328.
2000WO-US23328.
2000WO-US32678.
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2000WO-US13705.
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2000US-190828P
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2000US-1911AP
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2000WO-USO8439
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2000WS-187202P.
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2000US-189328P.
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                             Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood,
                                                                                                                                     when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; TANGO 361; transmembrane protein; diagnostic; asthma; immunological disorder; arthritis; graft rejection; renal disorder; acquired immunodeficiency syndrome; inflammatory disorders; psoriasis; AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour
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                                                                                                                                                                                                                                                                                                                    2 MYRPDVVRARKRVCWEDWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                               RSKTLGQSLRIVGGTEVEEGEWPWQASLQWDGSHACGATLINATWLVSAAHCFTTYKNPA
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                                                                                                                                                                                                                                                         Length 423;
                                                                                                                                                                                                                                                        Score 2255; DB 22;
Pred. No. 1.1e-178;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TANGO 361 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU01344 standard; Protein; 423 AA
           Claim 11; Fig 320; 774pp; English.
                                                                                                                                                                                                                                                        99.68;
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                   423 AA;
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GI 423
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Matches 420;
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prostate; cerebrovascular disease; pituitary; Cushing's disease;
neurodegenerative disease; Parkinson's disease.
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                                                                                                                                                                                                                                                                                       site"
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ce= "Protein kinase C phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
250..252
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/note= "Protein kinase C phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-myristyretto"
196..199
/note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Asn is N-glycosylated"
168..171
note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                    "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                 159..161
/note= "Protein kinase C phosphorylation
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/note= "ATP/GTP binding site motif"
360..365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192..417
/note= "Serine protease domain"
213..218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223..226
/note= "Asn is N-glycosylated"
228..233
                                                                                                                                                                                                                                                   'note= "Asn is N-glycosylated"
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/note= "Extracellular domain"
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371..375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "N-myristylation site"
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335..338
                                                                                                                                                                                  "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consensus sequence"
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                                                                                                                                                 "Mature TANGO 361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Serine protease,
                                                                                                               /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                       ..130
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standard; Protein; 423

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                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunodeficiency syndrome), inflammatory disorders (e.g. psoriasis and asthma), renal disorders, embryonic disorders, brain-related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischaemila), tumours, prostaterelated disorders, pituitary-related disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's disease).
                                                                                                                                         New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's disease
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                                                                                                                                                                                                           The sequence represents the amino acid sequence of human TANGO 361
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                                                                                             Kingsbury
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Pred. No. 1.1e-178;
1; Mismatches 1;
                                                                                             Barnes T,
                                                                                             Fraser CC,
                                                                                                                                                                                       Claim 8; Fig 13; 362pp; English.
                                                                                                                                                                                                                                                                                                                        tch 99.6%; al Similarity 99.5%; 420; Conservative
                                    20-SEP-2000; 2000WO-US25982.
                                                                          (MILL-) MILLENNIUM PHARM INC
                                                        99US-0399723
                                                                                             Sharp JD,
                                                                                                               WPI; 2001-211461/21
N-PSDB; AAS02070.
                                                                                                                                                                                                                                                                                                      423 AA;
WO200121631-A2
                                                        20-SEP-1999;
                  29-MAR-2001
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                                                                                            Kirst SJ,
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Best Local (
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The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as melecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DKLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski PJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.6%; Score 2255; DB 22; 99.5%; Pred. No. 1.1e-178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Fig 106; 278pp; English.
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99US-0169495.
99US-0170262.
2000US-0175481.
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2000WO-US04342.
2000WO-US04414.
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2000US-0187202.
2000US-0199397.
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J, Gurney AL,
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                                                                                                                         Human; PRO protein;
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18-FEB-2000;
22-FEB-2000;
                                                                                  Human PRO1461
                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                            24-AUG-2000;
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11-JAN-2000;
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                                       15-MAY-2001
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Matches 420;
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AAB87578;
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RESULT 6 AAB87578

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RESULT 7 **AAB66163**

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The nucleic acids may also be used in gene therapy
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                                                                                                                                                   Conservative
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                                                                                                                       Best Local Similarity
Matches 420; Conserv
                                                   423 AA
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GI 423
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                                                   Seguence
                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fong S;
Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents.
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                                                                                                                       RSKTLGQSLRIVGGTEVEEGEWPWQASLQWDGSHACGATLINATWLVSAAHCFTTYKNPA
                         Desnoyers L, Eaton DL, Ferrara N, owski PJ, Grimaldi CJ, Gurney AL, MA, Smith V, Stewart TA, Tumas D; PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted; transmembrane; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB66163 standard; protein; 423
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Goddard A, Godowski
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99US-0145698.
99US-0162506.
99WO-US28313.
99WO-US28551.
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16-DEC-1999; 99WO-US30095
05-JAN-2000; 2000WO-US00219
06-JAN-2000; 2000WO-US00376
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Pan J, Paoni NF, Roy MA,
Watanabe CK, Williams PM,
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29-OCT-1999;
30-NOV-1999;
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GI 423
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26-JUL-1999,
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Human; TANGO 361; transmembrane protein; diagnostic; asthma; immunological disorder; arthritis; graft rejection; renal disorder; acquired immunodeficiency syndrome; inflammatory disorders; psoriasis; AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pituitary; Cushing's disease;
                                                                                                                                                                                                                                                                                              ICRFHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                        SYEFQPGDVMFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRILCAGS 360
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                                                                                                                                 2 MYRPDVVRARKRVCWEDWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTT
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Score 2255; DB 22;
Pred. No. 1.1e-178;
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                                  Pred. No. 1.16
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                                                                                                    The sequence represents the amino acid sequence of human TANGO 361 variant #2 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunodeficiency syndrome), inflammatory disorders (e.g. psoriasis and asthma), renal disorders, embryonic disorders, brain-related disorders (e.g. crebral oedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate-related disorders, pituitary-related disorders (e.g. cushing's disease) and neurodegenerative diseases (e.g. Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; TANGO 361; transmembrane protein; diagnostic; asthma;
immunological disorder; arthritis; graft rejection; renal disorder;
acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
                     New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson'
                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                          Length 423;
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                                                                                                                                                                                                                                                           DB 22;
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                                                                                                                                                                                                                                                                      Pred. No. 2e-178;
2; Mismatches
                                                                                                                                                                                                                                                        Query Match 99.5%; Score 2252; Best Local Similarity 99.3%; Pred. No. 2e-Matches 419; Conservative 2; Mismatches
                                                                               Disclosure; Page 325-326; 362pp; English.
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N-PSDB; AAS02111
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The sequence represents the amino acid sequence of human TANGO 361 variant #3 transmembrane protein. The nucleic acid and polypeptide sequences are luseful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired asthma), renal disorders, embryonic disorders, brain-related disorders asthma), renal disorders, cerebral cedema), cerebrowscular diseases (e.g. ischaemia), tumnours, prostate-related disorders, pituitary-related disorders (e.g. cushing's disease) and neurodegenerative diseases (e.g. parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson'
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Pred. No. 2e-178;
2; Mismatches 1;
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99.38;
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Matches 419; Conserv
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                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variant #4 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunodeficiency syndrome), inflammatory disorders (e.g. psoriasis and asthma), renal disorders, embryonic disorders, brain-related disorders (e.g. cerebral oedema), cerebral oedema), cerebral disorders, pituitary related disorders (e.g. cushing's disease) and neurodegenerative diseases (e.g. parkinson's
                                                                                                                                                                                               Human; TANGO 361; transmembrane protein; diagnostic; asthma; immunological disorder; arthritis; graft rejection; renal disorder; acquired immunodeficiency syndrome; inflammatory disorders; psoriasis; AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pituitary; Cushing's disease; neurodegenerative disease; Parkinson's disease.
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                                                                                                                                                                    TANGO 361, variant #4 amino acid sequence.
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Pred. No. 2e-178;
2; Mismatches 1
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                                                                                AAU01402 standard; Protein; 423 AA
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New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human: TANGO 361; transmembrane protein; diagnostic; asthma; immunological disorder; arthritis; graft rejection; renal disorder; acquired immunodeficiency syndrome; inflammatory disorders; psoriasis; AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pituitary; Cushing's disease; neurodegenerative disease; Parkinson's disease
                                       RSKTLGQSLRIVGGTEVEEGEWPWQASLQWDGSHACGATLINATWLVSAAHCFTTYKNPA 240
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                                                      2 MYRPDVARARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTT 61
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                 carcinoma; prostate cancer; head; neck;
                                                                                                                                                                                      SYEFQPGDVMFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRILCAGS
                                                                                                                                                                                             1 MYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTT
                                                                                                                                RSKTLGQSLRIVGGTEVEEGEWPWQASLQWDGSHACGATLINATWLVSAAHCFTTYKNPA
                                                                                                                                                                                                                 LEGKTDACQGDSGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKT
                                 ö
                    Length 423;
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
19..37
/note= "Hydrophobic transmembrane region"
                                 Indels
                   Score 2251; DB 22;
Pred. No. 2.4e-178;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Catalytic domain"
                                                                                                                                                                                                                                                                                          AAY94709 standard; Protein; 422 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                       diagnosis; chromosome 4q12-4q13
                                                                                                                                                                                                                                                                                                                                  Human DESC1 protein variant #2.
                   99.5%;
                                                                                                                                                                                                                                                                                                                                                cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-IB01818
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                                                                                                                                                                                                                                                                                                                     (first entry)
                                 Conservative
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                          Similarity
      423 AA;
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                                                                                                                                                                                                                                                                                                                                                 Human; DESC1;
                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage-site
Domain
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-NOV-1999;
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GI 423
                                                                                                                                                                                                                                                                                                                     01-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-2000
                                                                                                                                                                                                                                            GI 422
                                 Matches 419;
      Sequence
                                                                                                                                                                                                                                                                                                        AAY94709
                   Query Match
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                            Local
                                                                                                                                                                                                                                                                                                                                                                                         Region
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This invention relates to a method for the diagnosis of squamous cell carcinoma or prostate cancer, comprising assaying for the expression of the DESC1 gene in the tissue sample from a subject. The present sequence represents the human DESC1 protein variant 2. The human DESC1 gene is located on chromosome 4q12-4q13, and the DESC1 protein has a predicted molecular weight of 44kD. The DESC1 gene is expressed in significant levels in epithelial derived tissue of the head, neck, oral mucosa, tonsils, prostate, testes and skin in healthy individuals. Tissue samples from patients with squamous cell carcinoma (particularly of the head and neck) do not express, or expresses at low levels the DESC1 gene.

Expression of the DESC1 gene is reduced or absent in prostate cancer. The DESC1 protein shows homology to serine protease family members. The methods of the invention can be used to diagnose squamous cell carcinoma methods of the invention can be used to diagnose squamous cell carcinoma cor prostate cancer in a tissue sample of a subject. The DESC1 cDNA is useful for producing DESC1 protein and for designing hybridization probes for isolating and identifying cDNA clones and genomic clones encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSKTLGQSLRIVGGTEVEEGEWPWQASLQWDGSHACGATLINATWLVSAAHCFTTYKNPA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWTASFGVTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPYTNAVHRVCLPDA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYEFOPGDVMFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRILCAGS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 LEGKTDACÓGDSGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDMITSKT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MYRPDVVRARKRVCWEPWVIGLVMFISLIVLAVCIGVTVHYVRYNOKKTYNYXSTLSFTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MYRPDVVRÄRKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTT 60
                                                                                             Diagnosing squamous cell carcinoma or prostate cancer especially squamous cell carcinomas of head and neck and tissues adjacent to tumor tissue comprises assaying for the expression of DESC1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE01946 standard; Protein; 422
                                                                                                                                                                                                                                          Claim 8; Fig 1B; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein or its allelic forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
2000-572035/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 417; Conserv
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                            N-PSDB; AAA28126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423
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GI 422
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comparing the corresponding nucleic acid molecules. An endotheliase domain and their corresponding nucleic acid molecules. An endotheliase protease domain of it is useful for the treatment and protease domain of it is useful for the treatment and classociated with aberrant angiogenesis or undesired neovascularisation. The undesired angiogenesis is associated with disorders selected from solid neoplasm, vascular malformations and cardiovascular disorders such as angiolibroma, angiolipoma, atherosclerosis, restenosis/reperfusion injury, arteriovenous malformations, haemangiomatosis and vascular adhesions, dyschondroplasia with vascular hamartomas (Fafucci's syndrome), hereditary haemorrhagic telangiectasia (Rendu-Osler-Weber syndrome) and von Hipple Lindau syndrome, chronic inflammatory diseases such as diabetes mellitus, haemophiliac joints, inflammatory disease, nonhealing fractures, periodonittis, psoriasis, inflammatory and arthritis, venous stasis ulcers, granulations-burns, hypertrophic scars, liver cirrhosis, osteoradionecrosis, postoperative adhesion, pyogenic granuloma and systemic solerosis, postoperative adhesion, pyogenic granuloma and systemic solerosis, postoperative adhesion, accordinatory disorders (Systemic solerosis, postoperative adhesion, accordinatory disorders (Systemic solerosis, postoperative adhesion, accordinatory disorders (Systemic solerodactyly and teangiectasis, dermatological disorders such as systemic vasculitis, scleroderma, pyoderma gangrenosum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is human endotheliase 1 protein which is encoded by DESC1 gene. DESC1 is used for the diagnosis of squamous cell carcinoma or
                                                                                                                                                                 crest syndrome; atherosclerosis; haemangiomatosis; diabetes mellitus; liver cirrhosis, osteoradionecrosis, systemic sclerosis; oseophageal; inflammatory bowel disease; fracture; rheumatoid arthritis; retinopathy; systemic vasculitis; scleroderma; neoplasm; ulcer; burn; DESC1 gene.
                                                                               Human; endothellase 1; protease domain; cytostatic; vulnerary; wound; nootzopic; periodontitis; dermatological disorder; gene therapy; scar; anglogenesis; cardiovascular disorder; psoriasis; neovascular disease; chronic inflammatory disease; occular disorder; circulatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a protein comprising endotheliase activity useful in the prevention and treatment of e.g. vascular malformations, cardiovascular disorders, and chronic inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190..422
/label= Protease_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Unknown
/note= "Encoded by TNG"
190. 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                by NTC"
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                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   'note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Encoded
                                                                                                                                                                                                                                                                                                                                                          /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Unknown
                                       Human endotheliase 1 protein
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(first entry)
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                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD05812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                             Homo sapiens
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31-JUL-2001
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        stains, blue rubber bleb nevus syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu syndrome and occular disorders such as blindness caused by occular neovascular disease, corneal graft neovascularisation,
 vasculopathy, venous, arterial ulcers, Sturge-Weber syndrome, Port-wine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protease; transgenic animal; transgenic non-human animal; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                  300
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                                                                                                                                                                                                                                               DKLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLL 120
                                                                                                                                                          Gaps
                                               macular degeneration, retinopathy of prematurity, retrolental fibroplasta and corneal neovascularisation. The nucleic acids of the invention are also used in gene therapy. The invention also provides method for screening compounds that modulate angiogenesis.
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                                                                                                                                                                                              ICRFHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTR
                                                                                                                                                                                                                                                                                                                                              1 MYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTT
                                                                                                                                                                                                                                                                                                                                                                                  RWTASFGVTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPYTNAVHRVCLPDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGKTDACQGDSGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKT
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                                                                                                                                     Length 422;
                                                                                                                                                          Indels
                                                                                                                                   DB 22;
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                                                                                                                                  Score 2232; DB 22;
Pred. No. 9.2e-177;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA021900 standard; Protein; 407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homologous human protease protein.
                                                                                                                                  98.68;
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2000US-0734675,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2002 (first entry)
                                                                                                                                              Best Local Similarity 98.8
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY
                                                                                                            422 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue typing.
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13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA021900;
                                                                                                            Sequence
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                  121
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                                                                                                                          The invention relates to a novel isolated human protease consisting or comprising of an amino acid sequence containing 405 amino acids fully defined in the specification, its allelic variant, orthologue or fragment. The human protease is useful for identifying a modulator of it, by contacting the human protease with an agent and determining if the agent has modulated the function, expression or activity of the human protease. A pharmaceutical composition of the invention is useful for treating a disease, or condition mediated by human protease. A human protease antibody is useful in tissue typing where a specific protein has been correlated with expression in specific tissue, antibodies that are specific for this protein which can be useful to identify a tissue type. The polynucleotide encoding the human protease is useful for constructing transgenic animals expressing the polynucleotide and peptides. A genetically engineered host cell is useful in producing a transgenic non-human animal, e.g. rodent such as rat or mouses, in which one or more of the cells of the animal include a transgene. This sequence represents a homologous protein of the human protease of the invention.
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                                                        Novel peptide designated as human protease useful as target for diagnosing a disease or predisposition to the disease mediated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 KRGLRRIIVHEKYKHPSHDYDISLAELSSPVPYTNAVHRVCLPDASYEFQPGDVMFVTGF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 TEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTEDPETVDK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 IVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVEEGEWPWQASLQWDGSHACGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKM 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRILCAGSLEGKTDACQGDSGGP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                16 EPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDKLYAEFGREASNNF 75
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0
                                                                                                                                                                                                                                                                                                                                                                     Length 407;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beasley EM;
                                                                                                                                                                                                                                                                                                                                                                     Score 2169; DB 23;
Pred. No. 1.5e-171;
1; Mismatches 1;
         Di Francesco V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human endotheliase 1 protease domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE01942 standard; Protein; 233 AA
                                                                                                       Disclosure; Fig 2; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                     95.8%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
         Webster M, Ketchum KA,
                               WPI; 2002-499867/53
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 405; Conserv
                                                                                                                                                                                                                                                                                                                                               407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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The present sequence is numnan encountained to protein, endotheliase proteins of protein or profease domain of it is useful for the treatment and domain and their corresponding nucleic acid molecules. An endotheliase protein or profease domain of it is useful for the treatment and diagnosis of disorders associated with aberrant analogenesis or undesired neovascularisation. The undesired angiogenesis is associated with aberrant analogenesis or undesired neovascular selected from solid neoplasm, vascular malformations and cardiovascular disorders such as angiofibroma, angiolipoma, and the mantion and cardiovascular paemorphasis and vascular malformations in a malformations heamonglomatosis and vascular adhesions, dyschondroplasis at the vascular hamartomas (Fafocci's syndrome), hereditary haemorrhagic telangiectasia (Rendu-Osler-Weber syndrome), hereditary haemorrhagic telangiectasia (Rendu-Osler-Weber syndrome) and von Hipple Lindau control inflammatory diseases such as diabetes mellitus, haemophiliac joints, inflammatory bowel disease, nonhealing fractures, cardiodertis; psoriasis, rheumatory bowel disease, nonhealing fractures, costeoradionecrosis, postoperative adhesion, pyogenic granulater systemic sclerosis and aberrant wound repairs, circulatory disorders systemic sclerosis and aberrant wound repairs, circulatory disorders such as systemic vasculitis, scleroderma, pyoderma quangrenosum, bushous the properties of the systemic varietis and teangiectasis, dermatological disorders such as systemic varietis and aberrant wound repairs, circulatory disorders such as systemic vasculitis, scleroderma, pyoderma quangrenosum, bushous as systemic varietis and aberrant scheroderma, pyoderma quangrenosum, bushous and attacked such as syndrome, bushous arterial uncers, sturge where syndrome, port whine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stains, blue tubber bleb nevus syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber: Rendu syndrome and occular disorders such as blindness caused by occular neovascular disease, corneal graft neovascularisation, macular degeneration, retinopathy of prematurity, retrolental
Human; endotheliase 1; protease domain; cytostatic; vulnerary; wound; nootropic; peridontitis; dermatological disorder; gene therapy; scar; anglogenesis; cardiovascular disorder; psoriasis; neovascular disease; chronic inflammatory disease, occular disorder; circulatory disorder; crest syndrome; atherosclerosis; haemangiomatosis; diabetes mellitus; liver cirrinosis, osteoradionecrosis, systemic sclerosis; oesophageal; inflammatory bowel disease; fracture; rheumatoid arthritis; retinopathy; systemic vasculitis; scleroderma; neoplasm; ulcer; burn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a protein comprising endotheliase activity useful in the prevention and treatment of e.g. vascular malformations, cardiovascular disorders, and chronic inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIVGGTEVEEGEWPWQASLQWDGSHACGATLINATWLVSAAHCFTTYKNPARWTASFGVT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibroplasia and corneal neovascularisation. The nucleic acids of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is human endotheliase 1 protease domain
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Pred. No. 9.8e-97;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.8%;
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22-SEP-2000; 2000US-0234840.
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N-PSDB; AAD05795.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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